



SEQUENCE LISTING

115

<110> Bertin, John
Manji, Gulam A.

<120> NOVEL MOLECULES OF THE PYRIN DOMAIN
PROTEIN FAMILY AND USES THEREOF

<130> 07334-341001

<140> US 10/027,629

<141> 2001-12-20

<150> US 09/964,955

<151> 2001-09-26

<150> US 09/653,901

<151> 2000-09-01

<150> US 09/506,067

<151> 2000-02-17

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Leu Ser Gln Asp Glu Leu Ser Lys Phe Lys Tyr Leu Ile Thr Thr Phe
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Ser Pro Ala His Glu Leu Gln Lys Ile Pro His Lys Glu Val Asp Lys
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Ala Asp Gly Lys Gln Leu Val Glu Ile Leu Thr Thr His Cys Asp Ser
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Thr Asp Leu Gln Glu Leu Leu Gly Cys Leu Tyr Glu Ser Gln Glu Glu				
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Leu Asn Ala Val Asp Val Val Pro Ser Ser Phe Cys Val Lys His Cys				
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Gly Ser Asn Lys Asp Leu Met Gly Leu Ala Ile Asn Asp Ser Phe Leu				
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agt gcc tcc cta gta agg atc ctg tgt gaa caa ata gcc tct gac acc				2174
Ser Ala Ser Leu Val Arg Ile Leu Cys Glu Gln Ile Ala Ser Asp Thr				
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Cys His Leu Gln Arg Val Val Phe Lys Asn Ile Ser Pro Ala Asp Ala				
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His Arg Asn Leu Cys Leu Ala Leu Arg Gly His Lys Thr Val Thr Tyr				
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ctg acc ctt caa ggc aat gac cag gat gat atg ttt ccc gca ttg tgt				2318
Leu Thr Leu Gln Gly Asn Asp Gln Asp Asp Met Phe Pro Ala Leu Cys				
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765	770	775	
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780	785	790	795
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800	805	810	
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815	820	825	
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830	835	840	
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845	850	855	
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910	915	920	
cca ctg tgc aac ttg aga tgt ctg tgg ttg tgg gga tgt tcc atc cct Pro Leu Cys Asn Leu Arg Cys Leu Trp Leu Trp Gly Cys Ser Ile Pro			2894
925	930	935	
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940	945	950	955
gtc act ctg gac ctg ggt cag aat ccc ttg ggg tct agt gga gtg aag Val Thr Leu Asp Leu Gly Gln Asn Pro Leu Gly Ser Ser Gly Val Lys			2990
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Tyr Lys Met Leu Ile Pro Phe Ser Asn Pro Arg Val Leu Pro Gly Pro		
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Phe Ser Tyr Thr Val Val Leu Tyr Gly Pro Ala Gly Leu Gly Lys Thr		
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His Lys Phe Lys Tyr Ala Phe Tyr Leu Ser Cys Arg Glu Leu Ser Arg		
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 Val Val Phe Lys Asn Ile Ser Pro Ala Asp Ala His Arg Asn Leu Cys

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755	760	765	
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120
171

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Leu Glu Asp Leu Glu Asp Val Asp Leu Lys Lys Phe Lys Met His Leu			
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gag gac tat cct ccc cag aag ggc tgc atc ccc ctc ccg agg ggt cag			267
Glu Asp Tyr Pro Pro Gln Lys Gly Cys Ile Pro Leu Pro Arg Gly Gin			
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aca gag aag gca gac cat gtg gat cta gcc acg cta atg atc gac ttc			315
Thr Glu Lys Ala Asp His Val Asp Leu Ala Thr Leu Met Ile Asp Phe			
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aat ggg gag gag aag gcg tgg gcc atg gcc gtg tgg atc ttc gct gcg			363
Asn Gly Glu Glu Lys Ala Trp Ala Met Ala Val Trp Ile Phe Ala Ala			
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atc aac agg aga gac ctt tat gag aaa gca aaa aga gat gag ccg aag			411
Ile Asn Arg Arg Asp Leu Tyr Glu Lys Ala Lys Arg Asp Glu Pro Lys			
80	85	90	
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Trp Gly Ser Asp Asn Ala Arg Val Ser Asn Pro Thr Val Ile Cys Gln			
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gaa gac agc att gaa gag gag tgg atg ggt tta ctg gag tac ctt tcg			507
Glu Asp Ser Ile Glu Glu Trp Met Gly Leu Leu Glu Tyr Leu Ser			
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aga atc tct att tgt aaa atg aag aaa gat tac cgt aag aag tac aga			555
Arg Ile Ser Ile Cys Lys Met Lys Lys Asp Tyr Arg Lys Lys Tyr Arg			
125	130	135	
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Lys Tyr Val Arg Ser Arg Phe Gln Cys Ile Glu Asp Arg Asn Ala Arg			
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ctg ggt gag agt gtg agc ctc aac aaa cgc tac aca cga ctg cgt ctc			651
Leu Gly Glu Ser Val Ser Leu Asn Lys Arg Tyr Thr Arg Leu Arg Leu			
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Ile Lys Glu His Arg Ser Gln Gln Glu Arg Glu Gln Glu Leu Leu Ala			
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Ile Gly Lys Thr Lys Thr Cys Glu Ser Pro Val Ser Pro Ile Lys Met			
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gag ttg ctg ttt gac ccc gat gat gag cat tct gag cct gtg cac acc			795
Glu Leu Leu Phe Asp Pro Asp Asp Glu His Ser Glu Pro Val His Thr			
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Val Val Phe Gln Gly Ala Ala Gly Ile Gly Lys Thr Ile Leu Ala Arg			

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240	245	250		
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255	260	265		
agg agc ctg ggg gac ctg atc atg agc tgc tgc ccc gac cca aac cca Arg Ser Leu Gly Asp Leu Ile Met Ser Cys Cys Pro Asp Pro Asn Pro				987
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ccc atc cac aag atc gtg aga aaa ccc tcc aga atc ctc ttc ctc atg Pro Ile His Lys Ile Val Arg Lys Pro Ser Arg Ile Leu Phe Leu Met				1035
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cgg cat gtg gag atc ctg ggt ttc tcc gag gcc aaa agg aaa gag tac Arg His Val Glu Ile Leu Gly Phe Ser Glu Ala Lys Arg Lys Glu Tyr				1275
365	370	375		
ttc ttc aag tac ttc tct gat gag gcc caa gcc agg gca gcc ttc agt Phe Phe Lys Tyr Phe Ser Asp Glu Ala Gln Ala Arg Ala Ala Phe Ser				1323
380	385	390	395	
ctg att cag gag aac gag gtc ctc ttc acc atg tgc ttc atc ccc ctg Leu Ile Gln Glu Asn Glu Val Leu Phe Thr Met Cys Phe Ile Pro Leu				1371
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415	420	425		
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430	435	440		
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445	450	455		

ctc tgc gcc cac ctc tgg ggg ctc tgc tct ttg gct gca gat gga atc Leu Cys Ala His Leu Trp Gly Leu Cys Ser Leu Ala Ala Asp Gly Ile 460 465 470 475	1563
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Asp Lys Gly Ile Lys Leu Leu Cys Glu Gly Leu Leu His Pro Asp Cys				
925	930	935		
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Lys Leu Gln Val Leu Glu Leu Asp Asn Cys Asn Leu Thr Ser His Cys				
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Cys Trp Asp Leu Ser Thr Leu Leu Thr Ser Ser Gln Ser Leu Arg Lys				
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Leu Ser Leu Gly Asn Asn Asp Leu Gly Asp Leu Gly Val Met Met Phe				
975	980	985		
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Cys Glu Val Leu Lys Gln Gln Ser Cys Leu Leu Gln Asn Leu Gly Leu				
990	995	1000		
tct gaa atg tat ttc aat tat gag aca aaa agt gcg tta gaa aca ctt				3195
Ser Glu Met Tyr Phe Asn Tyr Glu Thr Lys Ser Ala Leu Glu Thr Leu				
1005	1010	1015		
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His Val Asp Leu Ala Thr Leu Met Ile Asp Phe Asn Gly Glu Glu Lys
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 Thr Cys Glu Ser Pro Val Ser Pro Ile Lys Met Glu Leu Leu Phe Asp
 195 200 205
 Pro Asp Asp Glu His Ser Glu Pro Val His Thr Val Val Phe Gln Gly
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 Ile His Cys Arg Glu Val Ser Leu Val Thr Gln Arg Ser Leu Gly Asp
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 Leu Gln Gly Ala Phe Asp Glu His Ile Gly Pro Leu Cys Thr Asp Trp
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 Gln Lys Ala Glu Arg Gly Asp Ile Leu Leu Ser Ser Leu Ile Arg Lys
 325 330 335
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Phe Leu Phe Gly Leu Val Asn Gln Glu Arg Thr Ser Tyr Leu Glu Lys		
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Lys Leu Ser Cys Lys Ile Ser Gln Gln Ile Arg Leu Glu Leu Leu Lys		
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Trp Ile Glu Val Lys Ala Lys Ala Lys Leu Gln Ile Gln Pro Ser		
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Gln Leu Glu Leu Phe Tyr Cys Leu Tyr Glu Met Gln Glu Glu Asp Phe		
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Val Gln Arg Ala Met Asp Tyr Phe Pro Lys Ile Glu Ile Asn Leu Ser		640
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Thr Arg Met Asp His Met Val Ser Ser Phe Cys Ile Glu Asn Cys His		
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Arg Val Glu Ser Leu Ser Leu Gly Phe Leu His Asn Met Pro Lys Glu		
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Glu Glu Glu Glu Lys Glu Gly Arg His Leu Asp Met Val Gln Cys		
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Val Leu Pro Ser Ser Ser His Ala Ala Cys Ser His Gly Leu Val Asn		
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Ser His Leu Thr Ser Ser Phe Cys Arg Gly Leu Phe Ser Val Leu Ser		720
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Asp Pro Gly Met Arg Val Leu Cys Glu Thr Leu Gln His Pro Gly Cys		
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Gln Cys Asn Leu Gln Lys Leu Gly Leu Val Asn Ser Gly Leu Thr Ser		880
885	890	895
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Thr His Leu Tyr Leu Arg Gly Asn Thr Leu Gly Asp Lys Gly Ile Lys		
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Leu Leu Cys Glu Gly Leu Leu His Pro Asp Cys Lys Leu Gln Val Leu		
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Glu Leu Asp Asn Cys Asn Leu Thr Ser His Cys Cys Trp Asp Leu Ser		
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cacatggttt	tttccctttg	cattgagaac	tgtcatcggt	tttccctgggg	2040	
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<210> 7

<211> 77

<212> PRT

<213> Homo sapiens

<400> 7

Asp His Leu Leu Ser Thr	Leu Glu Glu	Leu Val Pro Tyr	Asp Phe Glu
1	5	10	15
Lys Phe Lys Phe Lys	Leu Gln Asn Thr	Ser Val Gln Lys	Glu His Ser
20	25	30	
Arg Ile Pro Arg Ser Gln	Ile Gln Arg Ala	Arg Pro Val Lys	Met Ala
35	40	45	
Thr Leu Leu Val Thr Tyr	Tyr Gly Glu Glu	Tyr Ala Val Gln	Leu Thr
50	55	60	
Leu Gln Val Leu Arg Ala	Ile Asn Gln Arg	Leu Leu Ala	
65	70	75	

<210> 8

<211> 77

<212> PRT

<213> Homo sapiens

<400> 8

Asp Ala Ile Leu Asp Ala	Leu Glu Asn Leu Thr	Ala Glu Glu	Leu Lys
1	5	10	15
Lys Phe Lys Leu Lys	Leu Leu Ser Val	Pro Leu Arg Glu	Gly Tyr Gly
20	25	30	
Arg Ile Pro Arg Gly Ala	Leu Leu Ser Met	Asp Ala Leu Asp	Leu Thr
35	40	45	
Asp Lys Leu Val Ser Phe	Tyr Leu Glu Thr Tyr	Gly Ala Glu Leu	Thr
50	55	60	
Ala Asn Val Leu Arg Asp	Met Gly Leu Gln Glu	Met Ala	
65	70	75	

<210> 9

<211> 77

<212> PRT

<213> Homo sapiens

<400> 9

Gly Arg Leu Ala Cys	Tyr Leu Glu Phe	Leu Lys Lys	Glu Glu Leu Lys
1	5	10	15
Glu Phe Gln Leu Leu	Leu Ala Asn Lys	Ala His Ser Arg	Ser Ser Ser
20	25	30	
Gly Glu Thr Pro Ala Gln	Pro Glu Lys	Thr Ser Gly	Met Glu Val Ala
35	40	45	

Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln Arg Ala Trp Asp Leu Ala
 50 55 60
 Leu His Thr Trp Glu Gln Met Gly Leu Arg Ser Leu Cys
 65 70 75

<210> 10
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<221> VARIANT
<222> (1)...(77)
<223> Xaa = Any Amino Acid

<400> 10
Asp Xaa Leu Leu Xaa Xaa Leu Glu Xaa Leu Xaa Xaa Glu Glu Leu Lys
 1 5 10 15
Lys Phe Lys Leu Leu Leu Xaa Asn Xaa Ser Xaa Xaa Glu Xaa Ser
 20 25 30
Arg Ile Pro Arg Xaa Gln Xaa Xaa Lys Ala Asp Gly Xaa Xaa Leu Ala
 35 40 45
Xaa Xaa Leu Val Thr Xaa Tyr Gly Glu Xaa Tyr Ala Val Glu Leu Ala
 50 55 60
Leu Gln Val Leu Glu Xaa Met Gly Leu Arg Xaa Leu Ala
 65 70 75

<210> 11
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<221> VARIANT
<222> (1)...(77)
<223> Xaa = Any Amino Acid

<400> 11
Asp Xaa Leu Ala Xaa Tyr Leu Glu Xaa Leu Xaa Xaa Glu Glu Leu Lys
 1 5 10 15
Lys Phe Lys Leu Leu Leu Xaa Asn Xaa Ser Pro Gln Lys Gly Xaa Ser
 20 25 30
Arg Ile Pro Arg Gly Gln Xaa Glu Lys Ala Asp Gly Val Asp Leu Ala
 35 40 45
Thr Leu Leu Val Thr Phe Tyr Gly Glu Glu Tyr Ala Trp Ala Leu Ala
 50 55 60
Leu Gln Val Leu Glu Ala Met Gly Leu Arg Asp Leu Ala
 65 70 75

<210> 12
<211> 28
<212> PRT
<213> Artificial Sequence

<220>

<223> Consensus sequence

<400> 12

Asn	Pro	Ser	Leu	Arg	Glu	Leu	Asp	Leu	Ser	Asn	Asn	Lys	Leu	Gly	Asp
1			5					10					15		
Glu	Gly	Ala	Arg	Ala	Leu	Ala	Glu	Ala	Leu	Lys	Ser				
			20					25							

<210> 13

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence

<400> 13

Asn	Leu	Glu	Glu	Leu	Asp	Leu	Ser	Asn	Asn	Leu	Thr	Ser	Leu	Pro	Pro
1				5				10					15		
Gly	Leu	Phe	Ser	Asn	Leu	Pro									
			20												

<210> 14

<211> 90

<212> PRT

<213> Homo sapiens

<400> 14

Met	Ala	Lys	Thr	Pro	Ser	Asp	His	Leu	Leu	Ser	Thr	Leu	Glu	Glu	Leu
1				5				10					15		
Val	Pro	Tyr	Asp	Phe	Glu	Lys	Phe	Lys	Phe	Lys	Leu	Gln	Asn	Thr	Ser
				20				25					30		
Val	Gln	Lys	Glu	His	Ser	Arg	Ile	Pro	Arg	Ser	Gln	Ile	Gln	Arg	Ala
				35			40					45			
Arg	Pro	Val	Lys	Met	Ala	Thr	Leu	Leu	Val	Thr	Tyr	Tyr	Gly	Glu	Glu
				50			55				60				
Tyr	Ala	Val	Gln	Leu	Thr	Leu	Gln	Val	Leu	Arg	Ala	Ile	Asn	Gln	Arg
				65			70			75			80		
Leu	Leu	Ala	Glu	Glu	Leu	His	Arg	Ala	Ala						
				85			90								

<210> 15

<211> 90

<212> PRT

<213> Homo sapiens

<400> 15

Met	Ala	Gly	Gly	Ala	Trp	Gly	Arg	Leu	Ala	Cys	Tyr	Leu	Glu	Phe	Leu
1				5				10					15		
Lys	Lys	Glu	Glu	Leu	Lys	Glu	Phe	Gln	Leu	Leu	Leu	Ala	Asn	Lys	Ala
				20				25					30		
His	Ser	Arg	Ser	Ser	Ser	Gly	Glu	Thr	Pro	Ala	Gln	Pro	Glu	Lys	Thr
				35			40					45			
Ser	Gly	Met	Glu	Val	Ala	Ser	Tyr	Leu	Val	Ala	Gln	Tyr	Gly	Glu	Gin
				50			55				60				

Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg
 65 70 75 80
 Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala
 85 90

<210> 16

<211> 89

<212> PRT

<213> Homo sapiens

<400> 16

Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
 1 5 10 15
 Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Ser Val Pro Leu
 20 25 30
 Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp
 35 40 45
 Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
 50 55 60
 Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
 65 70 75 80
 Met Ala Gly Gln Leu Gln Ala Ala Thr
 85

<210> 17

<211> 89

<212> PRT

<213> Homo sapiens

<400> 17

Met Gly Thr Lys Arg Glu Ala Ile Leu Lys Val Leu Glu Asn Leu Thr
 1 5 10 15
 Pro Glu Glu Leu Lys Lys Phe Lys Met Lys Leu Gly Thr Val Pro Leu
 20 25 30
 Arg Glu Gly Phe Glu Arg Ile Pro Arg Gly Ala Leu Gly Gln Leu Asp
 35 40 45
 Ile Val Asp Leu Thr Asp Lys Leu Val Ala Ser Tyr Tyr Glu Asp Tyr
 50 55 60
 Ala Ala Glu Leu Val Val Ala Val Leu Arg Asp Met Arg Met Leu Glu
 65 70 75 80
 Glu Ala Ala Arg Leu Gln Arg Ala Ala
 85